



## SEQUENCE LISTING

<110> YOSHIMURA, Koji  
HIKICHI, Yuichi  
NISHIMURA, Atsushi

<120> Novel Protein and DNA Thereof

<130> PF613TD1

<140> US 10/726,148

<141> 2003-12-02

<150> US 09/786,256

<151> 2001-03-02

<150> PCT/JP99/04766

<151> 1999-09-02

<150> JP 10-250115

<151> 1998-09-03

<160> 32

<170> PatentIn version 3.0

<210> 1

<211> 540

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(540)

<223> An isolated ADAM family protein

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Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr  
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Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu  
35 40 45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn  
50 55 60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala  
65 70 75 80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr  
85 90 95

Thr	Ser	Pro	Gln	Ile	Met	Asp	Asp	Cys	Tyr	Tyr	Gln	Gly	His	Ile	Leu		
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Asn	Glu	Lys	Val	Ser	Asp	Ala	Ser	Ile	Ser	Thr	Cys	Arg	Gly	Leu	Arg		
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Gly	Tyr	Phe	Ser	Gln	Gly	Asp	Gln	Arg	Tyr	Phe	Ile	Glu	Pro	Leu	Ser		
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Pro	Ile	His	Arg	Asp	Gly	Gln	Glu	His	Ala	Leu	Phe	Lys	Tyr	Asn	Pro		
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Asp	Glu	Lys	Asn	Tyr	Asp	Ser	Thr	Cys	Gly	Met	Asp	Gly	Val	Leu	Trp		
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Ala	His	Asp	Leu	Gln	Gln	Asn	Ile	Ala	Leu	Pro	Ala	Thr	Lys	Leu	Val		
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Lys	Leu	Lys	Asp	Arg	Lys	Val	Gln	Glu	His	Glu	Lys	Tyr	Ile	Glu	Tyr		
		195					200					205					
Tyr	Leu	Val	Leu	Asp	Asn	Gly	Glu	Phe	Lys	Arg	Tyr	Asn	Glu	Asn	Gln		
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Asp	Glu	Ile	Arg	Lys	Arg	Val	Phe	Glu	Met	Ala	Asn	Tyr	Val	Asn	Met		
225					230					235					240		
Leu	Tyr	Lys	Lys	Leu	Asn	Thr	His	Val	Ala	Leu	Val	Gly	Met	Glu	Ile		
			245					250						255			
Trp	Thr	Asp	Lys	Asp	Lys	Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Phe	Thr		
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Leu	Glu	Asn	Phe	Ser	Lys	Trp	Arg	Gly	Ser	Val	Leu	Ser	Arg	Arg	Lys		
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Arg	His	Asp	Ile	Ala	Gln	Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr		
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Thr	Val	Gly	Leu	Ala	Phe	Met	Ser	Thr	Met	Cys	Ser	Pro	Tyr	Ser	Val		
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Gly	Val	Val	Gln	Asp	His	Ser	Asp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr		
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Met	Ala	His	Glu	Met	Gly	His	Asn	Phe	Gly	Met	Phe	His	Asp	Asp	Tyr		
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Ser	Cys	Lys	Cys	Pro	Ser	Thr	Ile	Cys	Val	Met	Asp	Lys	Ala	Leu	Ser		
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Phe	Tyr	Ile	Pro	Thr	Asp	Phe	Ser	Ser	Cys	Ser	Arg	Leu	Ser	Tyr	Asp		
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Lys	Phe	Phe	Glu	Asp	Lys	Leu	Ser	Asn	Cys	Leu	Phe	Asn	Ala	Pro	Leu		
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Pro	Thr	Asp	Ile	Ile	Ser	Thr	Pro	Ile	Cys	Gly	Asn	Gln	Leu	Val	Glu		
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Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile  
 420 425 430  
 Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala  
 435 440 445  
 Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val  
 450 455 460  
 Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly  
 465 470 475 480  
 Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro  
 485 490 495  
 Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu  
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 <213> Homo sapiens

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 20 25 30  
 Ile Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys  
 35 40 45  
 Ala Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met  
 50 55 60  
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 65 70 75 80  
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 85 90 95

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 <213> Homo sapiens

<220>  
 <221> misc\_feature  
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 <223> Isolated DNA encoding for the protein of SEQ ID NO.1

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 gaactccctg ggggtgaagaa gtatgaagtg gtttataccta taagacttca tccactgcat 120  
 aaaagagagg ccaaagagcc agagcaacag gaacaatttg aaactgaatt aaagtataaa 180  
 atgacaatta atggaaaaaat tgcagtgtct tatttgaaaa aaaacaagaa cctccttgca 240  
 ccagggtaca cggaacata ttataattcc actggaaagg agatcaccac aagcccacaa 300  
 attatggatg attgttatta tcaaggacat attcttaatg aaaaggtttc tgacgctagc 360  
 atcagcacat gtaggggtct aaggggtctac ttcagtcagg gggatcaaag atactttatt 420  
 gaacctttta gccccatata tcgggatgga caggagcatg cactcttcaa gtataaccct 480  
 gatgaaaaga attatgacag cacctgtggg atggatgggtg tgttggtggc ccacgatttg 540  
 cagcagaaca ttgccctacc tgccaccaa ctagtaaaat tgaaagacag gaaggttcag 600  
 gaacatgaga aatacataga atattatttg gtcctggata atgggtgagtt taaaagggtac 660  
 aatgagaatc aagatgagat cagaaagagg gtatttgaga tggctaatta tgtcaacatg 720  
 ctttataaaa agctcaatac tcatgtggcc ttagtggta tggaaatctg gactgacaag 780  
 gataagataa agataacccc aaatgcaagc ttcaccttgg agaatttttc taaatggagg 840  
 gggagtgttc tctcaagaag aaagcgtcat gatattgtct agttaatcac agcaacagaa 900  
 cttgctggaa cgactgtggg tcttgcatth atgtctacaa tgtgttctcc ttattctgtt 960  
 ggcgttgttc aggaccacag cgataatctt cttagagttg cagggacaat ggcacatgaa 1020  
 atgggccaca actttggaat gtttcatgac gactattctt gcaagtgtcc ttctacaata 1080  
 tgtgtgatgg acaaagcact gagcttctat ataccacag acttcagttc ctgcagccgt 1140  
 ctgagctatg acaagttttt tgaagataaa ttatcaaatt gcctctttta tgctccattg 1200  
 cctacagata tcatatccac tccaatttgt gggaaaccagt tgggtggaaat gggagaggac 1260  
 tgtgatgttg ggacatctga ggaatgtacc aatatttgtt gtgatgctaa gacatgtaaa 1320  
 atcaaagcaa cttttcaatg tgcattagga gaatgttgtg aaaaatgcca atttaaaaag 1380  
 gctgggatgg tgtgcagacc agcaaaagat gagtgcgacc tgctgaaat gtgtaatggt 1440  
 aaatctggta attgtcctga tgatagattc caagtcaatg gcttcccttg ccatcacggg 1500  
 aagggccact gcttgatggg gacatgcccc acactgcagg agcagtgcac agagctgtgg 1560  
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 <213> Homo sapiens

<220>  
 <221> misc\_feature  
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 gactgtgatt gtgggacatc tgaggaatgt accaatatth gctgtgatgc taagacatgt 120  
 aaaatcaaag caacttttca atgtgcatta ggagaatgtt gtgaaaaatg ccaattttaa 180  
 aaggctggga tgggtgtcag accagcaaaa gatgagtgcg acctgcctga aatgtgtaat 240  
 ggtaaactctg gtaattgtcc tgatgataga ttccaagtca atggcttc 288

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 <212> PRT  
 <213> Homo sapiens

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 <222> (1)..(201)  
 <223> Isolated fragment of protein of SEQ ID NO.1 (aa 199-399)  
  
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 Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr Leu Val Leu Asp Asn  
 1 5 10 15  
 Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp Glu Ile Arg Lys Arg  
 20 25 30  
 Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu Tyr Lys Lys Leu Asn  
 35 40 45  
 Thr His Val Ala Leu Val Gly Met Glu Ile Trp Thr Asp Lys Asp Lys  
 50 55 60  
 Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu Glu Asn Phe Ser Lys  
 65 70 75 80  
 Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg His Asp Ile Ala Gln  
 85 90 95  
 Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr Thr Val Gly Leu Ala Phe  
 100 105 110  
 Met Ser Thr Met Cys Ser Pro Tyr Ser Val Gly Val Val Gln Asp His  
 115 120 125  
 Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met Ala His Glu Met Gly  
 130 135 140  
 His Asn Phe Gly Met Phe His Asp Asp Tyr Ser Cys Lys Cys Pro Ser  
 145 150 155 160  
 Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe Tyr Ile Pro Thr Asp  
 165 170 175  
 Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys Phe Phe Glu Asp Lys  
 180 185 190  
 Leu Ser Asn Cys Leu Phe Asn Ala Pro  
 195 200  
  
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 <213> Homo sapiens  
  
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 <222> (1)..(10)  
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 Glu Cys Thr Asn Ile Cys Cys Asp Ala Lys

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atcacagtcc tctccattt ccaccaac		28
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 ggaaccagtt ggtggaaatg ggagagga 28  
  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> (1)..(775)  
 <223> An isolated ADAM family protein

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 Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu  
 35 40 45  
 Gln Gln Glu Gln Trp Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn  
 50 55 60  
 Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala  
 65 70 75 80  
 Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr  
 85 90 95  
 Thr Ser Pro Gln Ile Met Trp Trp Trp Tyr Tyr Gln Gly His Ile Leu  
 100 105 110  
 Asn Glu Lys Val Ser Trp Ala Ser Ile Ser Thr Trp Arg Gly Leu Arg  
 115 120 125  
 Gly Tyr Trp Ser Gln Gly Trp Gln Arg Tyr Trp Ile Glu Pro Leu Ser  
 130 135 140  
 Pro Ile His Arg Trp Gly Gln Glu His Ala Leu Trp Lys Tyr Asn Pro  
 145 150 155 160  
 Trp Glu Lys Asn Tyr Trp Ser Thr Trp Gly Met Trp Gly Val Leu Trp  
 165 170 175  
 Ala His Trp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val  
 180 185 190  
 Lys Leu Lys Trp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr  
 195 200 205  
 Tyr Leu Val Leu Trp Asn Gly Glu Trp Lys Arg Tyr Asn Glu Asn Gln  
 210 215 220  
 Trp Glu Ile Arg Lys Arg Val Trp Glu Met Ala Asn Tyr Val Asn Met  
 225 230 235 240  
 Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile  
 245 250 255



Trp	Thr	Trp	Lys	Trp	Lys	Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Trp	Thr		
			260					265					270				
Leu	Glu	Asn	Trp	Ser	Lys	Trp	Arg	Gly	Ser	Val	Leu	Ser	Arg	Arg	Lys		
		275					280					285					
Arg	His	Trp	Ile	Ala	Gln	Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr		
	290					295					300						
Thr	Val	Gly	Leu	Ala	Trp	Met	Ser	Thr	Met	Trp	Ser	Pro	Tyr	Ser	Val		
305					310					315					320		
Gly	Val	Val	Gln	Trp	His	Ser	Trp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr		
			325					330						335			
Met	Ala	His	Glu	Met	Gly	His	Asn	Trp	Gly	Met	Trp	His	Trp	Trp	Tyr		
			340					345					350				
Ser	Trp	Lys	Trp	Pro	Ser	Thr	Ile	Trp	Val	Met	Trp	Lys	Ala	Leu	Ser		
		355					360					365					
Trp	Tyr	Ile	Pro	Thr	Trp	Trp	Ser	Ser	Trp	Ser	Arg	Leu	Ser	Tyr	Trp		
	370					375					380						
Lys	Trp	Trp	Glu	Trp	Lys	Leu	Ser	Asn	Trp	Leu	Trp	Asn	Ala	Pro	Leu		
385					390					395					400		
Pro	Thr	Trp	Ile	Ile	Ser	Thr	Pro	Ile	Trp	Gly	Asn	Gln	Leu	Val	Glu		
			405						410					415			
Met	Gly	Glu	Trp	Trp	Trp	Trp	Gly	Thr	Ser	Glu	Glu	Trp	Thr	Asn	Ile		
		420					425						430				
Trp	Trp	Trp	Ala	Lys	Thr	Trp	Lys	Ile	Lys	Ala	Thr	Trp	Gln	Trp	Ala		
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Leu	Gly	Glu	Trp	Trp	Glu	Lys	Trp	Gln	Trp	Lys	Lys	Ala	Gly	Met	Val		
	450					455					460						
Trp	Arg	Pro	Ala	Lys	Trp	Glu	Trp	Trp	Leu	Pro	Glu	Met	Trp	Asn	Gly		
465					470					475					480		
Lys	Ser	Gly	Asn	Trp	Pro	Trp	Trp	Arg	Trp	Gln	Val	Asn	Gly	Trp	Pro		
			485					490						495			
Trp	His	His	Gly	Lys	Gly	His	Trp	Leu	Met	Gly	Thr	Trp	Pro	Thr	Leu		
			500				505						510				
Gln	Glu	Gln	Trp	Thr	Glu	Leu	Trp	Gly	Pro	Gly	Thr	Glu	Val	Ala	Trp		
		515					520					525					
Lys	Ser	Trp	Tyr	Asn	Arg	Asn	Glu	Gly	Gly	Ser	Lys	Tyr	Gly	Tyr	Trp		
	530					535					540						
Arg	Arg	Val	Trp	Trp	Thr	Leu	Ile	Pro	Trp	Lys	Ala	Asn	Trp	Thr	Met		
545					550					555					560		
Trp	Gly	Lys	Leu	Trp	Trp	Gln	Gly	Gly	Ser	Trp	Asn	Leu	Pro	Trp	Lys		
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Gly Arg Ile Val Thr Trp Leu Thr Trp Lys Thr Trp Trp Pro Glu Trp  
 580 585 590  
 Thr Ser Gln Glu Ile Gly Met Val Ala Asn Gly Thr Lys Trp Gly Trp  
 595 600 605  
 Asn Lys Val Trp Ile Asn Ala Glu Trp Val Trp Ile Glu Lys Ala Tyr  
 610 615 620  
 Lys Ser Thr Asn Trp Ser Ser Lys Trp Lys Gly His Ala Val Trp Trp  
 625 630 635 640  
 His Glu Leu Gln Trp Gln Trp Glu Glu Gly Trp Ile Pro Pro Trp Trp  
 645 650 655  
 Trp Trp Ser Ser Val Val Trp His Trp Ser Ile Val Val Gly Val Leu  
 660 665 670  
 Trp Pro Met Ala Val Ile Trp Val Val Val Ala Met Val Ile Arg His  
 675 680 685  
 Gln Ser Ser Arg Glu Lys Gln Lys Lys Trp Gln Arg Pro Leu Ser Thr  
 690 695 700  
 Thr Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met Val Lys  
 705 710 715 720  
 Ala Val Gln Pro Gln Glu Met Ser Gln Met Lys Pro His Val Tyr Trp  
 725 730 735  
 Leu Pro Val Glu Gly Asn Glu Pro Pro Ala Ser Trp His Lys Trp Thr  
 740 745 750  
 Asn Ala Leu Pro Pro Thr Val Trp Lys Trp Asn Pro Met Ser Thr Pro  
 755 760 765  
 Lys Trp Ser Asn Pro Lys Ala  
 770 775

<210> 16  
 <211> 2325  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(2325)  
 <223> Isolated nucleic acid encoding for a protein of SEQ ID NO. 15

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 aaaagagagg ccaaagagcc agagcaacag gaacaatttg aaactgaatt aaagtataaa 180  
 atgacaatta atggaaaaat tgcagtgctt tatttgaaaa aaaacaagaa cctccttgca 240  
 ccaggctaca cggaaacata ttataattcc actggaaagg agatcaccac aagcccacaa 300  
 attatggatg attgttatta tcaaggacat attcttaatg aaaagggttc tgacgctagc 360  
 atcagcacat gtaggggtct aaggggctac ttcagtcagg gggatcaaag atactttatt 420  
 gaacctttta gccccatata tcgggatgga caggagcatg cactcttcaa gtataaccct 480

gatgaaaaga	attatgacag	cacctgtggg	atggatgggtg	tgttgtgggc	ccacgatttg	540
cagcagaaca	ttgccctacc	tgccaccaaa	ctagtaaaat	tgaaagacag	gaaggttcag	600
gaacatgaga	aatacataga	atattatttg	gtcctggata	atggtgagtt	taaaaggtag	660
aatgagaatc	aagatgagat	cagaaagagg	gtatttgaga	tggctaatta	tgtcaacatg	720
ctttataaaa	agctcaatac	tcatgtggcc	ttagttggta	tggaaatctg	gactgacaag	780
gataagataa	agataacccc	aaatgcaagc	ttcaccttgg	agaatttttc	taaatggagg	840
gggagtgttc	tctcaagaag	aaagcgtcat	gatattgctc	agttaatcac	agcaacagaa	900
cttgctggaa	cgactgtggg	tcttgcatth	atgtctacaa	tgtgttctcc	ttattctgth	960
ggcgttgthc	aggaccacag	cgataatctt	cttagagttg	cagggacaat	ggcacatgaa	1020
atggggccaca	actttggaat	gtttcatgac	gactattctt	gcaagtgtcc	ttctacaata	1080
tgtgtgatgg	acaaagcact	gagcttctat	ataccacacag	acttcagthc	ctgcagccgt	1140
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tgtgattgtg	ggacatctga	ggaatgtacc	aatatttgct	gtgatgctaa	gacatgtaaa	1320
atcaaagcaa	ctthttcaatg	tgcattagga	gaatgttgtg	aaaaatgcca	atttaaaaag	1380
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aaatctggta	attgtcctga	tgatagattc	caagtcaatg	gcttcccttg	ccatcacggg	1500
aagggccact	gcttgatggg	gacatgcccc	acactgcagg	agcagtgcac	agaactgtgg	1560
ggaccaggaa	ctgaggttgc	agataagtca	tgttacaaca	ggaatgaagg	tgggtcaaag	1620
tacgggtact	gtcgcagagt	ggatgacaca	ctcattccct	gcaaagcaaa	tgataccatg	1680
tgtgggaagt	tgttctgtca	aggtgggtcg	gataatttgc	cctggaaagg	acggatagtg	1740
actttcctga	catgtaaaac	atttgatcct	gaagacacaa	gtcaagaaat	aggcatggtg	1800
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gtggttgcta	tggtaatccg	gcaccagagc	tccagagaaa	agcagaagaa	agatcagagg	2100
ccactatcta	ccactggcac	caggccacac	aaacagaaga	ggaaacccca	gatggtaaaag	2160
gctgttcaac	cccaagagat	gagtcagatg	aagccccatg	tgtatgatct	gccagtagaa	2220
ggcaatgagc	ccccagcctc	ttttcataaa	gacacaaacg	cacttcccc	tactgttttc	2280
aaggataatc	caatgtctac	acctaaggac	tcaaattcaa	aagca		2325

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<220>  
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<400> 17  
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<210> 18  
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 <212> DNA  
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<400> 18  
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<210> 19

<211> 24  
 <212> DNA  
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<220>  
 <223> Nucleic Acid Primer

<400> 19  
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<210> 20  
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 <212> DNA  
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<220>  
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<400> 20  
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<210> 21  
 <211> 28  
 <212> DNA  
 <213> Artificial sequence

<220>  
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<400> 21  
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<210> 22  
 <211> 24  
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<210> 23  
 <211> 30  
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<210> 24  
 <211> 29  
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<220>  
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<400> 24  
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<210> 25  
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<220>  
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<400> 25  
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<210> 26  
 <211> 28  
 <212> DNA  
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<220>  
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<400> 26  
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<210> 27  
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<220>  
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<400> 27  
 cgccgctggg ctgccgggtc 20

<210> 28  
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<213> Artificial sequence

<220>

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<400> 28

tccatccccga tgtatggggc

20

<210> 29

<211> 2560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55)..(1674)

<220>

<221> misc\_feature

<222> (1)..(2560)

<223> DNA sequence of FIG 1-2 containing SEQ ID NO:3 encoding for protein of SEQ ID NO:1

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<221> mat\_peptide

<222> (55)..()

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Met  
1

57

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Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Ser Val Ala Val Ser  
5 10 15

105

gct ata aaa gaa ctc cct ggg gtg aag aag tat gaa gtg gtt tat cct  
Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr Pro  
20 25 30

153

ata aga ctt cat cca ctg cat aaa aga gag gcc aaa gag cca gag caa  
Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu Gln  
35 40 45

201

cag gaa caa ttt gaa act gaa tta aag tat aaa atg aca att aat gga  
Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn Gly  
50 55 60 65

249

aaa att gca gtg ctt tat ttg aaa aaa aac aag aac ctc ctt gca cca  
Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala Pro  
70 75 80

297

ggc tac acg gaa aca tat tat aat tcc act gga aag gag atc acc aca  
Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr Thr  
85 90 95

345

agc cca caa att atg gat gat tgt tat tat caa gga cat att ctt aat	393
Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu Asn	
100 105 110	
gaa aag gtt tct gac gct agc atc agc aca tgt agg ggt cta agg ggc	441
Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg Gly	
115 120 125	
tac ttc agt cag ggg gat caa aga tac ttt att gaa cct tta agc ccc	489
Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser Pro	
130 135 140 145	
ata cat cgg gat gga cag gag cat gca ctc ttc aag tat aac cct gat	537
Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro Asp	
150 155 160	
gaa aag aat tat gac agc acc tgt ggg atg gat ggt gtg ttg tgg gcc	585
Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp Ala	
165 170 175	
cac gat ttg cag cag aac att gcc cta cct gcc acc aaa cta gta aaa	633
His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val Lys	
180 185 190	
ttg aaa gac agg aag gtt cag gaa cat gag aaa tac ata gaa tat tat	681
Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr	
195 200 205	
ttg gtc ctg gat aat ggt gag ttt aaa agg tac aat gag aat caa gat	729
Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp	
210 215 220 225	
gag atc aga aag agg gta ttt gag atg gct aat tat gtc aac atg ctt	777
Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu	
230 235 240	
tat aaa aag ctc aat act cat gtg gcc tta gtt ggt atg gaa atc tgg	825
Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile Trp	
245 250 255	
act gac aag gat aag ata aag ata acc cca aat gca agc ttc acc ttg	873
Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu	
260 265 270	
gag aat ttt tct aaa tgg agg ggg agt gtt ctc tca aga aga aag cgt	921
Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg	
275 280 285	
cat gat att gct cag tta atc aca gca aca gaa ctt gct gga acg act	969
His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr Thr	
290 295 300 305	
gtg ggt ctt gca ttt atg tct aca atg tgt tct cct tat tct gtt ggc	1017
Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val Gly	
310 315 320	
gtt gtt cag gac cac agc gat aat ctt ctt aga gtt gca ggg aca atg	1065
Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met	
325 330 335	

gca cat gaa atg ggc cac aac ttt gga atg ttt cat gac gac tat tct	1113
Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr Ser	
340 345 350	
tgc aag tgt cct tct aca ata tgt gtg atg gac aaa gca ctg agc ttc	1161
Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe	
355 360 365	
tat ata ccc aca gac ttc agt tcc tgc agc cgt ctc agc tat gac aag	1209
Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys	
370 375 380 385	
ttt ttt gaa gat aaa tta tca aat tgc ctc ttt aat gct cca ttg cct	1257
Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu Pro	
390 395 400	
aca gat atc ata tcc act cca att tgt ggg aac cag ttg gtg gaa atg	1305
Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu Met	
405 410 415	
gga gag gac tgt gat tgt ggg aca tct gag gaa tgt acc aat att tgc	1353
Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile Cys	
420 425 430	
tgt gat gct aag aca tgt aaa atc aaa gca act ttt caa tgt gca tta	1401
Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala Leu	
435 440 445	
gga gaa tgt tgt gaa aaa tgc caa ttt aaa aag gct ggg atg gtg tgc	1449
Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val Cys	
450 455 460 465	
aga cca gca aaa gat gag tgc gac ctg cct gaa atg tgt aat ggt aaa	1497
Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly Lys	
470 475 480	
tct ggt aat tgt cct gat gat aga ttc caa gtc aat ggc ttc cct tgc	1545
Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro Cys	
485 490 495	
cat cac ggg aag ggc cac tgc ttg atg ggc aca tgc ccc aca ctg cag	1593
His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu Gln	
500 505 510	
gag cag tgc aca gag ctg tgg gga cca ggt agg agg aca aat cct ttc	1641
Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Arg Arg Thr Asn Pro Phe	
515 520 525	
ccc tgt gca tgt gcg aag gaa aat cat ttc aga tgacagtgtt taaccatggt	1694
Pro Cys Ala Cys Ala Lys Glu Asn His Phe Arg	
530 535 540	
caaaggacca ttctgtccta tccttcttag aagcttcgaa ctcaaaaatca tggaaagggt	1754
ttaagatttg aggttggtt tagggttgct agatttagca agtaaaaaata aggatggccc	1814
cgttaaat ttaacttaaaa ttaacaagtt ttttggttaat tttttgtttt ttgtctcagc	1874
atcagtatat cccatgcaat acttgagggtg tgctcactact aaaattat tttgtatctga	1934
aattcaaatt aaactgggtg tctttttctt ttcattctggc aaccctacta agatcataaa	1994
cccttggaaa tctgtgtgtg tgcgggtgtg tgtgtgtgtg tgtgtgcagg ggtggcagaa	2054
gtactgtggg atgggacaga aataagaaaa gatggaaaaa agaaaaagaac tctggaaatg	2114



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cagaaagcca ataaagaaaa gtgaaagttc ttaaattggc gctttgtcca taatgccaaa 2174
atttttagaga ccatattctc taatttcacc aagaaaactt gaaaaataaa agtttaaaga 2234
gatatccgaa aatttaaaca gcaatttgta tagtattaaa taactttggc caggtgcggt 2294
ggctcacacc tgtaatccca gcactttggg aggctgaggc gggcggatca cgaggtcagg 2354
agatcaagac catcctggct arcacggtga aaccccgctc ctactaaaaa tacaaaaaat 2414
tagccgggcg tgctagtggg cgctgtccc agctactcgg gaggtgagg caggagaagg 2474
gcctgaaccc aggaggcgga gcttgccgct agcagagatc gtgccactgc actccagcct 2534
gggtgacaaa gccagactcc gtttcc 2560

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<212> PRT
<213> Homo sapiens

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<220>
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<223> DNA sequence of FIG 1-2 containing SEQ ID NO:3 encoding for protein
      of SEQ ID NO:

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<400> 30

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Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr
      20              25              30

Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
      35              40              45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn
50              55              60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala
65              70              75              80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr
      85              90              95

Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu
100              105              110

Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg
115              120              125

Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser
130              135              140

Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro
145              150              155              160

Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp
165              170              175

Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
180              185              190

```

Lys	Leu	Lys	Asp	Arg	Lys	Val	Gln	Glu	His	Glu	Lys	Tyr	Ile	Glu	Tyr	195	200	205	
Tyr	Leu	Val	Leu	Asp	Asn	Gly	Glu	Phe	Lys	Arg	Tyr	Asn	Glu	Asn	Gln	210	215	220	
Asp	Glu	Ile	Arg	Lys	Arg	Val	Phe	Glu	Met	Ala	Asn	Tyr	Val	Asn	Met	225	230	235	240
Leu	Tyr	Lys	Lys	Leu	Asn	Thr	His	Val	Ala	Leu	Val	Gly	Met	Glu	Ile	245	250	255	
Trp	Thr	Asp	Lys	Asp	Lys	Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Phe	Thr	260	265	270	
Leu	Glu	Asn	Phe	Ser	Lys	Trp	Arg	Gly	Ser	Val	Leu	Ser	Arg	Arg	Lys	275	280	285	
Arg	His	Asp	Ile	Ala	Gln	Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr	290	295	300	
Thr	Val	Gly	Leu	Ala	Phe	Met	Ser	Thr	Met	Cys	Ser	Pro	Tyr	Ser	Val	305	310	315	320
Gly	Val	Val	Gln	Asp	His	Ser	Asp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr	325	330	335	
Met	Ala	His	Glu	Met	Gly	His	Asn	Phe	Gly	Met	Phe	His	Asp	Asp	Tyr	340	345	350	
Ser	Cys	Lys	Cys	Pro	Ser	Thr	Ile	Cys	Val	Met	Asp	Lys	Ala	Leu	Ser	355	360	365	
Phe	Tyr	Ile	Pro	Thr	Asp	Phe	Ser	Ser	Cys	Ser	Arg	Leu	Ser	Tyr	Asp	370	375	380	
Lys	Phe	Phe	Glu	Asp	Lys	Leu	Ser	Asn	Cys	Leu	Phe	Asn	Ala	Pro	Leu	385	390	395	400
Pro	Thr	Asp	Ile	Ile	Ser	Thr	Pro	Ile	Cys	Gly	Asn	Gln	Leu	Val	Glu	405	410	415	
Met	Gly	Glu	Asp	Cys	Asp	Cys	Gly	Thr	Ser	Glu	Glu	Cys	Thr	Asn	Ile	420	425	430	
Cys	Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys	Ala	435	440	445	
Leu	Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met	Val	450	455	460	
Cys	Arg	Pro	Ala	Lys	Asp	Glu	Cys	Asp	Leu	Pro	Glu	Met	Cys	Asn	Gly	465	470	475	480
Lys	Ser	Gly	Asn	Cys	Pro	Asp	Asp	Arg	Phe	Gln	Val	Asn	Gly	Phe	Pro	485	490	495	
Cys	His	His	Gly	Lys	Gly	His	Cys	Leu	Met	Gly	Thr	Cys	Pro	Thr	Leu	500	505	510	

Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Arg Arg Thr Asn Pro  
515 520 525

Phe Pro Cys Ala Cys Ala Lys Glu Asn His Phe Arg  
530 535 540

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<212> DNA  
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<222> (55)..(2379)

<220>  
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<222> (55)..()

<220>  
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of SEQ ID NO:1

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Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val Ser  
5 10 15

gct ata aaa gaa ctc cct ggg gtg aag aag tat gaa gtg gtt tat cct 153  
Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr Pro  
20 25 30

ata aga ctt cat cca ctg cat aaa aga gag gcc aaa gag cca gag caa 201  
Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu Gln  
35 40 45

cag gaa caa ttt gaa act gaa tta aag tat aaa atg aca att aat gga 249  
Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn Gly  
50 55 60 65

aaa att gca gtg ctt tat ttg aaa aaa aac aag aac ctc ctt gca cca 297  
Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala Pro  
70 75 80

ggc tac acg gaa aca tat tat aat tcc act gga aag gag atc acc aca 345  
Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr Thr  
85 90 95

agc cca caa att atg gat gat tgt tat tat caa gga cat att ctt aat 393  
Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu Asn

100	105	110	
gaa aag gtt tct gac gct agc atc agc aca tgt agg ggt cta agg ggc Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg Gly 115 120 125			441
tac ttc agt cag ggg gat caa aga tac ttt att gaa cct tta agc ccc Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser Pro 130 135 140 145			489
ata cat cgg gat gga cag gag cat gca ctc ttc aag tat aac cct gat Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro Asp 150 155 160			537
gaa aag aat tat gac agc acc tgt ggg atg gat ggt gtg ttg tgg gcc Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp Ala 165 170 175			585
cac gat ttg cag cag aac att gcc cta cct gcc acc aaa cta gta aaa His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val Lys 180 185 190			633
ttg aaa gac agg aag gtt cag gaa cat gag aaa tac ata gaa tat tat Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr 195 200 205			681
ttg gtc ctg gat aat ggt gag ttt aaa agg tac aat gag aat caa gat Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp 210 215 220 225			729
gag atc aga aag agg gta ttt gag atg gct aat tat gtc aac atg ctt Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu 230 235 240			777
tat aaa aag ctc aat act cat gtg gcc tta gtt ggt atg gaa atc tgg Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile Trp 245 250 255			825
act gac aag gat aag ata aag ata acc cca aat gca agc ttc acc ttg Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu 260 265 270			873
gag aat ttt tct aaa tgg agg ggg agt gtt ctc tca aga aga aag cgt Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg 275 280 285			921
cat gat att gct cag tta atc aca gca aca gaa ctt gct gga acg act His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr Thr 290 295 300 305			969
gtg ggt ctt gca ttt atg tct aca atg tgt tct cct tat tct gtt ggc Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val Gly 310 315 320			1017
gtt gtt cag gac cac agc gat aat ctt ctt aga gtt gca ggg aca atg Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met 325 330 335			1065
gca cat gaa atg ggc cac aac ttt gga atg ttt cat gac gac tat tct Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr Ser			1113

340	345	350	
tgc aag tgt cct tct aca ata tgt gtg atg gac aaa gca ctg agc ttc Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe 355 360 365			1161
tat ata ccc aca gac ttc agt tcc tgc agc cgt ctc agc tat gac aag Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys 370 375 380 385			1209
ttt ttt gaa gat aaa tta tca aat tgc ctc ttt aat gct cca ttg cct Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu Pro 390 395 400			1257
aca gat atc ata tcc act cca att tgt ggg aac cag ttg gtg gaa atg Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu Met 405 410 415			1305
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tgt gat gct aag aca tgt aaa atc aaa gca act ttt caa tgt gca tta Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala Leu 435 440 445			1401
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aga cca gca aaa gat gag tgc gac ctg cct gaa atg tgt aat ggt aaa Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly Lys 470 475 480			1497
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cat cac ggg aag ggc cac tgc ttg atg ggg aca tgc ccc aca ctg cag His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu Gln 500 505 510			1593
gag cag tgc aca gag ctg tgg gga cca gga act gag gtt gca gat aag Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Thr Glu Val Ala Asp Lys 515 520 525			1641
tca tgt tac aac agg aat gaa ggt ggg tca aag tac ggg tac tgt cgc Ser Cys Tyr Asn Arg Asn Glu Gly Gly Ser Lys Tyr Gly Tyr Cys Arg 530 535 540 545			1689
aga gtg gat gac aca ctc att ccc tgc aaa gca aat gat acc atg tgt Arg Val Asp Asp Thr Leu Ile Pro Cys Lys Ala Asn Asp Thr Met Cys 550 555 560			1737
ggg aag ttg ttc tgt caa ggt ggg tgc gat aat ttg ccc tgg aaa gga Gly Lys Leu Phe Cys Gln Gly Gly Ser Asp Asn Leu Pro Trp Lys Gly 565 570 575			1785
cgg ata gtg act ttc ctg aca tgt aaa aca ttt gat cct gaa gac aca			1833

Arg	Ile	Val	Thr	Phe	Leu	Thr	Cys	Lys	Thr	Phe	Asp	Pro	Glu	Asp	Thr		
		580					585					590					
agt	caa	gaa	ata	ggc	atg	gtg	gcc	aat	gga	act	aag	tgt	ggc	gat	aac	1881	
Ser	Gln	Glu	Ile	Gly	Met	Val	Ala	Asn	Gly	Thr	Lys	Cys	Gly	Asp	Asn		
	595					600					605						
aag	gtt	tgc	att	aat	gca	gaa	tgt	gtg	gat	att	gag	aaa	gcc	tac	aaa	1929	
Lys	Val	Cys	Ile	Asn	Ala	Glu	Cys	Val	Asp	Ile	Glu	Lys	Ala	Tyr	Lys		
610					615					620					625		
tca	acc	aat	tgc	tca	tct	aag	tgc	aaa	gga	cat	gct	gtg	tgt	gac	cat	1977	
Ser	Thr	Asn	Cys	Ser	Ser	Lys	Cys	Lys	Gly	His	Ala	Val	Cys	Asp	His		
				630					635					640			
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gac	tcc	tca	gtg	gtc	ttc	cac	ttc	tcc	att	gtg	gtt	ggg	gtg	ctg	ttc	2073	
Asp	Ser	Ser	Val	Val	Phe	His	Phe	Ser	Ile	Val	Val	Gly	Val	Leu	Phe		
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cca	atg	gcg	gtc	att	ttt	gtg	gtg	gtt	gct	atg	gta	atc	cgg	cac	cag	2121	
Pro	Met	Ala	Val	Ile	Phe	Val	Val	Val	Ala	Met	Val	Ile	Arg	His	Gln		
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agc	tcc	aga	gaa	aag	cag	aag	aaa	gat	cag	agg	cca	cta	tct	acc	act	2169	
Ser	Ser	Arg	Glu	Lys	Gln	Lys	Lys	Asp	Gln	Arg	Pro	Leu	Ser	Thr	Thr		
690					695				700						705		
ggc	acc	agg	cca	cac	aaa	cag	aag	agg	aaa	ccc	cag	atg	gta	aag	gct	2217	
Gly	Thr	Arg	Pro	His	Lys	Gln	Lys	Arg	Lys	Pro	Gln	Met	Val	Lys	Ala		
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gtt	caa	ccc	caa	gag	atg	agt	cag	atg	aag	ccc	cat	gtg	tat	gat	ctg	2265	
Val	Gln	Pro	Gln	Glu	Met	Ser	Gln	Met	Lys	Pro	His	Val	Tyr	Asp	Leu		
			725					730						735			
cca	gta	gaa	ggc	aat	gag	ccc	cca	gcc	tct	ttt	cat	aaa	gac	aca	aac	2313	
Pro	Val	Glu	Gly	Asn	Glu	Pro	Pro	Ala	Ser	Phe	His	Lys	Asp	Thr	Asn		
		740					745					750					
gca	ctt	ccc	cct	act	gtt	ttc	aag	gat	aat	cca	atg	tct	aca	cct	aag	2361	
Ala	Leu	Pro	Pro	Thr	Val	Phe	Lys	Asp	Asn	Pro	Met	Ser	Thr	Pro	Lys		
	755					760					765						
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Asp	Ser	Asn	Pro	Lys	Ala												
770					775												
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 of SEQ ID NO:1

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Pro	Ile	Arg	Leu	His	Pro	Leu	His	Lys	Arg	Glu	Ala	Lys	Glu	Pro	Glu	35	40	45	
Gln	Gln	Glu	Gln	Phe	Glu	Thr	Glu	Leu	Lys	Tyr	Lys	Met	Thr	Ile	Asn	50	55	60	
Gly	Lys	Ile	Ala	Val	Leu	Tyr	Leu	Lys	Lys	Asn	Lys	Asn	Leu	Leu	Ala	65	70	75	80
Pro	Gly	Tyr	Thr	Glu	Thr	Tyr	Tyr	Asn	Ser	Thr	Gly	Lys	Glu	Ile	Thr	85	90	95	
Thr	Ser	Pro	Gln	Ile	Met	Asp	Asp	Cys	Tyr	Tyr	Gln	Gly	His	Ile	Leu	100	105	110	
Asn	Glu	Lys	Val	Ser	Asp	Ala	Ser	Ile	Ser	Thr	Cys	Arg	Gly	Leu	Arg	115	120	125	
Gly	Tyr	Phe	Ser	Gln	Gly	Asp	Gln	Arg	Tyr	Phe	Ile	Glu	Pro	Leu	Ser	130	135	140	
Pro	Ile	His	Arg	Asp	Gly	Gln	Glu	His	Ala	Leu	Phe	Lys	Tyr	Asn	Pro	145	150	155	160
Asp	Glu	Lys	Asn	Tyr	Asp	Ser	Thr	Cys	Gly	Met	Asp	Gly	Val	Leu	Trp	165	170	175	
Ala	His	Asp	Leu	Gln	Gln	Asn	Ile	Ala	Leu	Pro	Ala	Thr	Lys	Leu	Val	180	185	190	
Lys	Leu	Lys	Asp	Arg	Lys	Val	Gln	Glu	His	Glu	Lys	Tyr	Ile	Glu	Tyr	195	200	205	
Tyr	Leu	Val	Leu	Asp	Asn	Gly	Glu	Phe	Lys	Arg	Tyr	Asn	Glu	Asn	Gln	210	215	220	
Asp	Glu	Ile	Arg	Lys	Arg	Val	Phe	Glu	Met	Ala	Asn	Tyr	Val	Asn	Met	225	230	235	240

Leu	Tyr	Lys	Lys	Leu	Asn	Thr	His	Val	Ala	Leu	Val	Gly	Met	Glu	Ile	
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Trp	Thr	Asp	Lys	Asp	Lys	Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Phe	Thr	
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Leu	Glu	Asn	Phe	Ser	Lys	Trp	Arg	Gly	Ser	Val	Leu	Ser	Arg	Arg	Lys	
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Arg	His	Asp	Ile	Ala	Gln	Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr	
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Thr	Val	Gly	Leu	Ala	Phe	Met	Ser	Thr	Met	Cys	Ser	Pro	Tyr	Ser	Val	
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Gly	Val	Val	Gln	Asp	His	Ser	Asp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr	
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Met	Ala	His	Glu	Met	Gly	His	Asn	Phe	Gly	Met	Phe	His	Asp	Asp	Tyr	
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Ser	Cys	Lys	Cys	Pro	Ser	Thr	Ile	Cys	Val	Met	Asp	Lys	Ala	Leu	Ser	
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Phe	Tyr	Ile	Pro	Thr	Asp	Phe	Ser	Ser	Cys	Ser	Arg	Leu	Ser	Tyr	Asp	
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Lys	Phe	Phe	Glu	Asp	Lys	Leu	Ser	Asn	Cys	Leu	Phe	Asn	Ala	Pro	Leu	
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Met	Gly	Glu	Asp	Cys	Asp	Cys	Gly	Thr	Ser	Glu	Glu	Cys	Thr	Asn	Ile	
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Cys	Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys	Ala	
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Leu	Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met	Val	
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Cys	Arg	Pro	Ala	Lys	Asp	Glu	Cys	Asp	Leu	Pro	Glu	Met	Cys	Asn	Gly	
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Lys	Ser	Gly	Asn	Cys	Pro	Asp	Asp	Arg	Phe	Gln	Val	Asn	Gly	Phe	Pro	
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Cys	His	His	Gly	Lys	Gly	His	Cys	Leu	Met	Gly	Thr	Cys	Pro	Thr	Leu	
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Gln	Glu	Gln	Cys	Thr	Glu	Leu	Trp	Gly	Pro	Gly	Thr	Glu	Val	Ala	Asp	
		515					520					525				
Lys	Ser	Cys	Tyr	Asn	Arg	Asn	Glu	Gly	Gly	Ser	Lys	Tyr	Gly	Tyr	Cys	
	530					535					540					
Arg	Arg	Val	Asp	Asp	Thr	Leu	Ile	Pro	Cys	Lys	Ala	Asn	Asp	Thr	Met	
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Cys	Gly	Lys	Leu	Phe	Cys	Gln	Gly	Gly	Ser	Asp	Asn	Leu	Pro	Trp	Lys	
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Gly	Arg	Ile	Val	Thr	Phe	Leu	Thr	Cys	Lys	Thr	Phe	Asp	Pro	Glu	Asp	
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Thr	Ser	Gln	Glu	Ile	Gly	Met	Val	Ala	Asn	Gly	Thr	Lys	Cys	Gly	Asp	
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Asn	Lys	Val	Cys	Ile	Asn	Ala	Glu	Cys	Val	Asp	Ile	Glu	Lys	Ala	Tyr	
	610					615					620					
Lys	Ser	Thr	Asn	Cys	Ser	Ser	Lys	Cys	Lys	Gly	His	Ala	Val	Cys	Asp	
625					630					635					640	
His	Glu	Leu	Gln	Cys	Gln	Cys	Glu	Glu	Gly	Trp	Ile	Pro	Pro	Asp	Cys	
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Asp	Asp	Ser	Ser	Val	Val	Phe	His	Phe	Ser	Ile	Val	Val	Gly	Val	Leu	
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Phe	Pro	Met	Ala	Val	Ile	Phe	Val	Val	Val	Ala	Met	Val	Ile	Arg	His	
		675					680					685				
Gln	Ser	Ser	Arg	Glu	Lys	Gln	Lys	Lys	Asp	Gln	Arg	Pro	Leu	Ser	Thr	
	690					695					700					
Thr	Gly	Thr	Arg	Pro	His	Lys	Gln	Lys	Arg	Lys	Pro	Gln	Met	Val	Lys	
705					710					715					720	
Ala	Val	Gln	Pro	Gln	Glu	Met	Ser	Gln	Met	Lys	Pro	His	Val	Tyr	Asp	
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Leu	Pro	Val	Glu	Gly	Asn	Glu	Pro	Pro	Ala	Ser	Phe	His	Lys	Asp	Thr	
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Asn	Ala	Leu	Pro	Pro	Thr	Val	Phe	Lys	Asp	Asn	Pro	Met	Ser	Thr	Pro	
	755						760					765				
Lys	Asp	Ser	Asn	Pro	Lys	Ala										
	770					775										